



SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> 1889/00401

<140> 09/833,017

<141> 2001-04-10

<160> 30

<170> PatentIn version 3.0

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<211> 141

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(141)

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48

gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt
Asp Glu Leu Glu Ile Ile Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

96

ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa
Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

141

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<212> PRT

<213> Streptococcus mutans

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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 <213> Streptococcus mutans

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Gln Ala Leu Gly Lys
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acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
 Thr Val Leu Phe Leu Leu Phe Ser Lys Val Ser Asn Val Thr
 20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata
 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
 35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
 50 55 60

 cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
 65 70 75 80

 ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
 85 90 95

 ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336
 Leu Phe Arg Arg Ala Ile Ile Phe Ile Leu Asp Gly Thr Gln Gly
 100 105 110

 att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca 384
 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
 115 120 125

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cont
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 Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
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 165 170 175

 ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt 576
 Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
 180 185 190

 aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca 624
 Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
 195 200 205

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 210 215 220

 caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata 720
 Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
 225 230 235 240

 gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat 768
 Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
 245 250 255

 att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt 816
 Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
 260 265 270

 att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg 864

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
 275 280 285

cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat 912
 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
 290 295 300

gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa 960
 Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
 305 310 315 320

aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag 1008
 Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
 325 330 335

atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat 1056
 Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
 340 345 350

gcc att gag gct ttc gaa tca tta aat cct gaa att cag tta gcc 1104
 Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
 355 360 365

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 370 375 380

aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc 1200
 Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
 385 390 395 400

act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att 1248
 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
 405 410 415

ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat 1296
 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
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tta ttc aag caa ctc cta ata ata aaa tag 1326
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 <213> Streptococcus mutans

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Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
 20 25 30

cont

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
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Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
100 105 110

Cont Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
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Leu Phe Lys Gln Leu Leu Ile Ile Lys
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 ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat 96
 Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
 20 25 30

 aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc 144
 Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
 35 40 45

 cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa 192
 Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
 50 55 60

 aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat 240
 Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
 65 70 75 80

 aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg 288
 Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
 85 90 95

 ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa 336
 Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
 100 105 110

Cont
 tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat 384
 Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
 115 120 125

 tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt 432
 Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
 130 135 140

 att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att 480
 Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
 145 150 155 160

 ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act 528
 Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
 165 170 175

 tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa 576
 Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
 180 185 190

 atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct 624
 Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
 195 200 205

 gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga 672
 Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
 210 215 220

aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga 720
Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
225 230 235 240

gct gtg att gct gat caa agg aga gca aaa 750
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245 250

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<212> PRT
<213> Streptococcus mutans

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Met Ile Ser Ile Phe Val Leu Glu Asp Asp Phe Leu Gln Gln Gly Arg
1 5 10 15

Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
20 25 30

Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
35 40 45

Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
50 55 60

Cheat
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
65 70 75 80

Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
85 90 95

Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
100 105 110

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
180 185 190

Met Asp Lys Arg-Leu Phe Gln-Cys-His-Arg Ser Phe Ile Val-Asn-Pro
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
210 215 220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
225 230 235 240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
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1 5 10 15

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<222> (1)..(46)

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala
35 40

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Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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Orients

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Ceotic

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 <222> (1)..(408)

<400> 24

atg	gaa	gaa	gat	ttt	gaa	att	gtt	ttt	aat	aag	gtt	aag	cca	att	gta		48
Met	Glu	Glu	Asp	Phe	Glu	Ile	Val	Phe	Asn	Lys	Val	Lys	Pro	Ile	Val		
1	5							10					15				

tgg	aaa	tta	agc	cgt	tat	tac	ttt	att	aaa	atg	tgg	act	cgt	gaa	gat		96
Trp	Lys	Leu	Ser	Arg	Tyr	Tyr	Phe	Ile	Lys	Met	Trp	Thr	Arg	Glu	Asp		
20		25							30								

Cont.

tgg	caa	caa	gag	gga	atg	ttg	att	ttg	cac	caa	tta	tta	agg	gaa	cat		144
Trp	Gln	Gln	Glu	Gly	Met	Leu	Ile	Leu	His	Gln	Leu	Leu	Arg	Glu	His		
35		40							45								

cca	gaa	tta	gaa	gag	gat	aca	aaa	ttg	tat	atc	tat	ttt	aag	aca		192
Pro	Glu	Leu	Glu	Asp	Asp	Thr	Lys	Leu	Tyr	Ile	Tyr	Phe	Lys	Thr		
50		55						60								

cgt	ttt	tct	aat	tac	att	aaa	gat	gtt	ttg	cgt	cag	caa	gaa	agt	cag		240
Arg	Phe	Ser	Asn	Tyr	Ile	Lys	Asp	Val	Leu	Arg	Gln	Gln	Glu	Ser	Gln		
65		70						75			80						

aaa	cgt	cgt	ttt	aat	aga	atg	tct	tat	gaa	gaa	gtc	ggt	gag	att	gaa		288
Lys	Arg	Arg	Phe	Asn	Arg	Met	Ser	Tyr	Glu	Glu	Val	Gly	Glu	Ile	Glu		
85			90						95								

cac	tgt	ttg	tca	agt	ggc	ggt	atg	caa	ttg	gat	gaa	tat	att	tta	ttt		336
His	Cys	Leu	Ser	Ser	Gly	Gly	Met	Gln	Leu	Asp	Glu	Tyr	Ile	Leu	Phe		
100					105							110					

cgt	gat	agt	ttg	ctt	gca	tat	aaa	caa	ggt	ctg	agt	act	gaa	aag	caa		384
Arg	Asp	Ser	Leu	Leu	Ala	Tyr	Lys	Gln	Gly	Leu	Ser	Thr	Glu	Lys	Gln		
115			120						125								

gag	ctg	ttt	gag	cgc	ttg	gta	gca	ggagagcact	ttttggaaag	gcaaagtatg		438
-----	-----	-----	-----	-----	-----	-----	-----	------------	------------	------------	--	-----

Glu Leu Phe Glu Arg Leu Val Ala
130 135

ctgaaagatt tacgtaaaaa attaagtat tttaaggaaa aa 480

<210> 25
<211> 136
<212> PRT
<213> Streptococcus mutans

<400> 25

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val
1 5 10 15

Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

Cleat
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala
130 135

<210> 26
<211> 680
<212> DNA
<213> Streptococcus mutans

<220>
<221> misc_feature
<222> (1)..(680)

<400> 26
gtaaataaaa cagccagtta agatggaca tttatgtcct gttcttaaag tcttttcgt 60
tttataataa ttttattata aaaggaggc atcgtaatag atggaagaat atttgaaat 120
tgttttaat aaggtaagc caattgtatg gaaattaagc cgttattact ttattaaaat 180
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240
acatccagaa tttagaagagg atgataaaaa attgtatatac tatttaaga cacgttttc 300
taattacatt aaagatgttt tgctcagca agaaagtcag aaacgtcgtt ttaatagaat 360
gtcttatgaa gaagtcggtg agattgaaca ctgttgtca agtggcggtt tgcaattgga 420
tgaatatatt ttatttcgt atagtttgct tgcataaaaa caaggtctga gtactgaaaa 480
gcaagagctg tttgagcgct tggtagcagg agagcactt ttggaaaggc aaagtatgct 540
gaaagattta cgtaaaaaat taagtgattt taagaaaaaa tagttaaaaaa gggaaagaat 600
ggaacatgtg attgtaccat tcttttggt tgaaaattaa gaaaagttat tataaattat 660
tggtttaaca tgccatatta 680

CDS
<210> 27
<211> 2280
<212> DNA
<213> Streptococcus mutans

<220>
<221> CDS
<222> (1)..(2280)

<400> 27
atg aaa caa gtt att tat gtt gtt tta atc gtc ata gcc gtt aac att 48
Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct 240
Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
65 70 75 80

tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt 288
 Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
 85 90 95

 ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc 336
 Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
 100 105 110

 aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt 384
 Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
 115 120 125

 atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc 432
 Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
 130 135 140

 tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca 480
 Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
 145 150 155 160

 gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca 528
 Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
 165 170 175

 ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa 576
 Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
 180 185 190

C1
Cat
 ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag 624
 Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
 195 200 205

 aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc 672
 Lys Ala Leu Met Thr Tyr Ile Ile Ala Ser Leu Ile Val Thr Leu
 210 215 220

 att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac 720
 Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
 225 230 235 240

 att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg 768
 Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
 245 250 255

 ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac 816
 Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
 260 265 270

 ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct 864
 Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
 275 280 285

 tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg 912
 Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
 290 295 300

 cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att 960

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
 305 310 315 320
 gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg
 Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
 325 330 335
 1008
 gta att ttg gtt ggt ggg gtt ttg gcg caa aac aat aac ctt ttc
 Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
 340 345 350
 1056
 ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct
 Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
 355 360 365
 1104
 ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat
 Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
 370 375 380
 1152
 gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc
 Ala Val Val Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
 385 390 395 400
 1200
 att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt
 Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
 405 410 415
 1248
 gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt
 Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
 420 425 430
 1296
 gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt
 Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445
 1344
 gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca
 Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460
 1392
 gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat
 Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480
 1440
 cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc
 Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495
 1488
 gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt
 Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510
 1536
 gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att
 Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
 515 520 525
 1584
 tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta
 Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
 530 535
 1632

530	535	540	
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545	550	555	1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565	570	575	1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580	585	590	1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595	600	605	1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610	615	620	1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625	630	635	1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645	650	655	1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660	665	670	2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675	680	685	2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690	695	700	2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705	710	715	2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln 725	730	735	2208
gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln 740	745	750	2256
ggt ttc tat tat aac ctg ttt aat Gly Phe Tyr Tyr Asn Leu Phe Asn 755	760		2280

C'ant

<210> 28
<211> 760
<212> PRT
<213> Streptococcus mutans

<400> 28

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Cont

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr-Leu Gln Gly Ile-Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Clint Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser

420

425

430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
580 585 590

�oncise
Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 29
<211> 900
<212> DNA
<213> Streptococcus mutans

<220>
<221> CDS
<222> (1)...(900)

Scart
<400> 29
atg gat cct aaa ttt tta caa agt gca gaa ttt tat agg aga cgc tat 48
Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Tyr
1 5 10 15

cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc 96
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att 144
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct 192
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct 240

Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala			
65	70	75	80
gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca			288
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro			
85	90	95	
aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga			336
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg			
100	105	110	
gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag			384
Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys			
115	120	125	
tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac			432
Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp			
130	135	140	
aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att			480
Lys Glu Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile			
145	150	155	160
ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt			528
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly			
165	170	175	
gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat			576
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp			
180	185	190	
att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat			624
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp			
195	200	205	
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa			672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu			
210	215	220	
aaa aag gga aat gac aag gtt gtt att gaa gga aaa att aac aat gtc			720
Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val			
225	230	235	240
gct tca tca gca act act aaa aaa gga aat ctc ttt aag gtt act			768
Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr			
245	250	255	
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt			816
Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly			
260	265	270	
atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat			864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp			
275	280	285	
tat ttc aaa gat aaa tta ctg cat aaa atg gat aat			900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn			

1
Cont

290

295

300

<210> 30

<211> 300

<212> PRT

<213> Streptococcus mutans

<400> 30

Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
1 5 10 15

His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

cont
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65 70 75 80

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
85 90 95

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
100 105 110

Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp
130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

ChorC. Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
290 295 300